(ii) obtaining sequence information from the termini of each of said plurality of clones, thereby obtaining a pair of terminal sequences;

(iii) identifying a pair of sequences within said reference genome that corresponds to each of said pairs of terminal sequences; and

(iv) determining the relationship between the members of each pair of corresponding sequences within said reference genome;

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wherein a difference in the observed relationship between the members of any of said pairs of corresponding sequences within said reference genome and the expected relationship based upon said known size of said plurality of clones indicates the presence of a rearrangement in said test genome compared to said reference genome and wherein said test genome is obtained from an individual with a disease associated with chromosomal rearrangements.

Please add new claims 24-25 as follows:

24. (New) The method of claim 1, wherein the determining step (iv) comprises determining the genetic or physical distance the pair of sequences.

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25. (New) The method of claim 1, wherein the determining step (iv) comprises determining whether the pair of sequences are present in the same vector or chromosome.

REMARKS

1. Status of the claims

With entry of this amendment, claim 1 is amended and claims 24 and 25 are added. Claims 1-25 are pending with entry of the Amendment.

A marked up copy of the amended claims are provided as Appendix A entitled "**VERSION WITH MARKINGS TO SHOW CHANGES MADE.**" As a convenience to the Examiner, a complete set of the claims, as amended herein, is also attached to this Amendment as Appendix B.